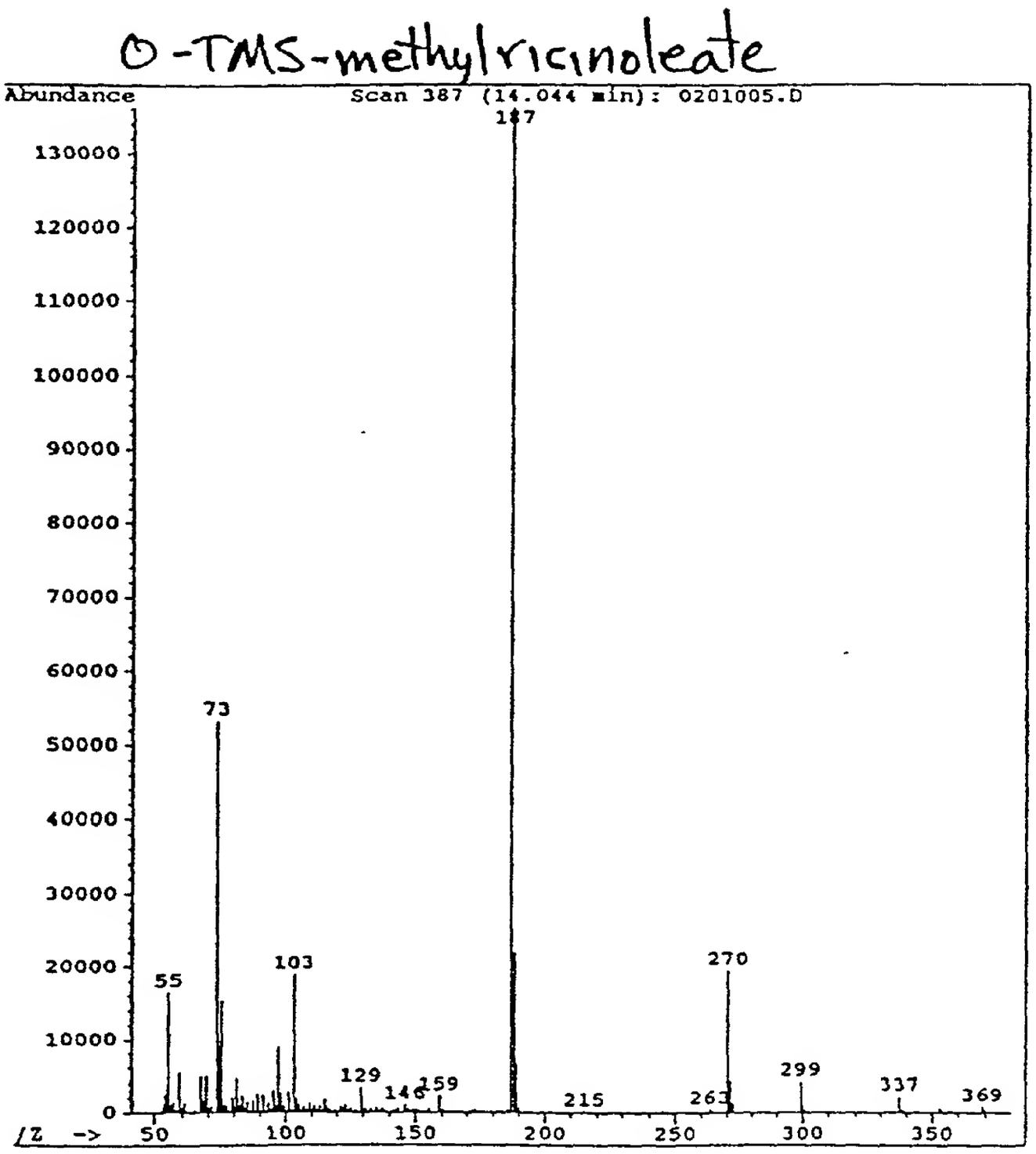
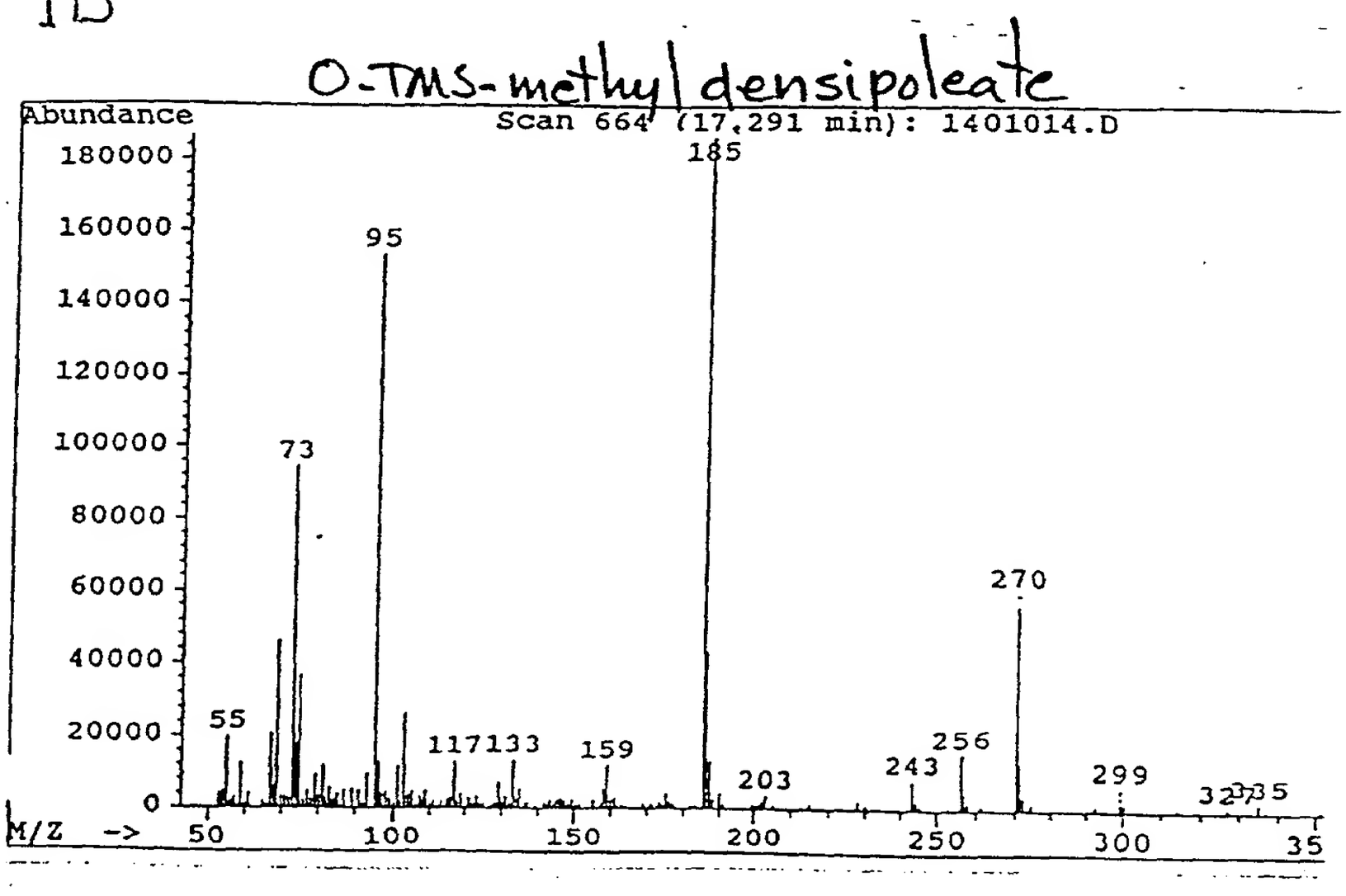
Figure 1A

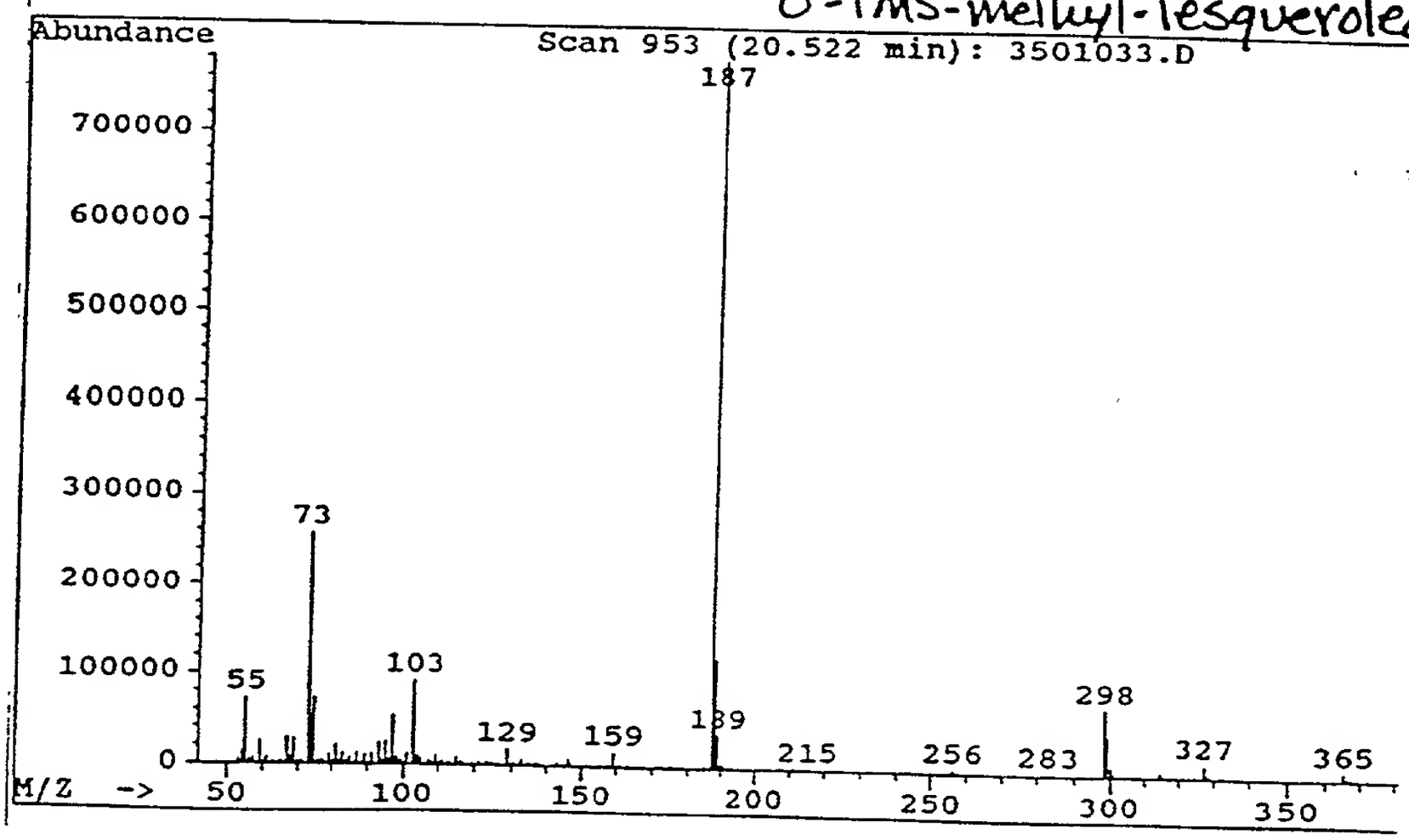

O-TMS-methylricinoleate
Abundance
Scan 387 (14.044 min): 0201005.D
187
130000
120000
110000
100000
90000
80000
70000
60000
50000
40000
30000
20000
10000
0
73
55
103
129
146
159
215
263
270
299
337
369
/z -> 50 100 150 200 250 300 350

1B


O-TMS-methyldensipoleate
Abundance
Scan 664 (17.291 min): 1401014.D
185
180000
160000
140000
120000
100000
80000
60000
40000
20000
0
95
73
55
117133
159
203
243
256
270
299
M/Z -> 50 100 150 200 250 300 35

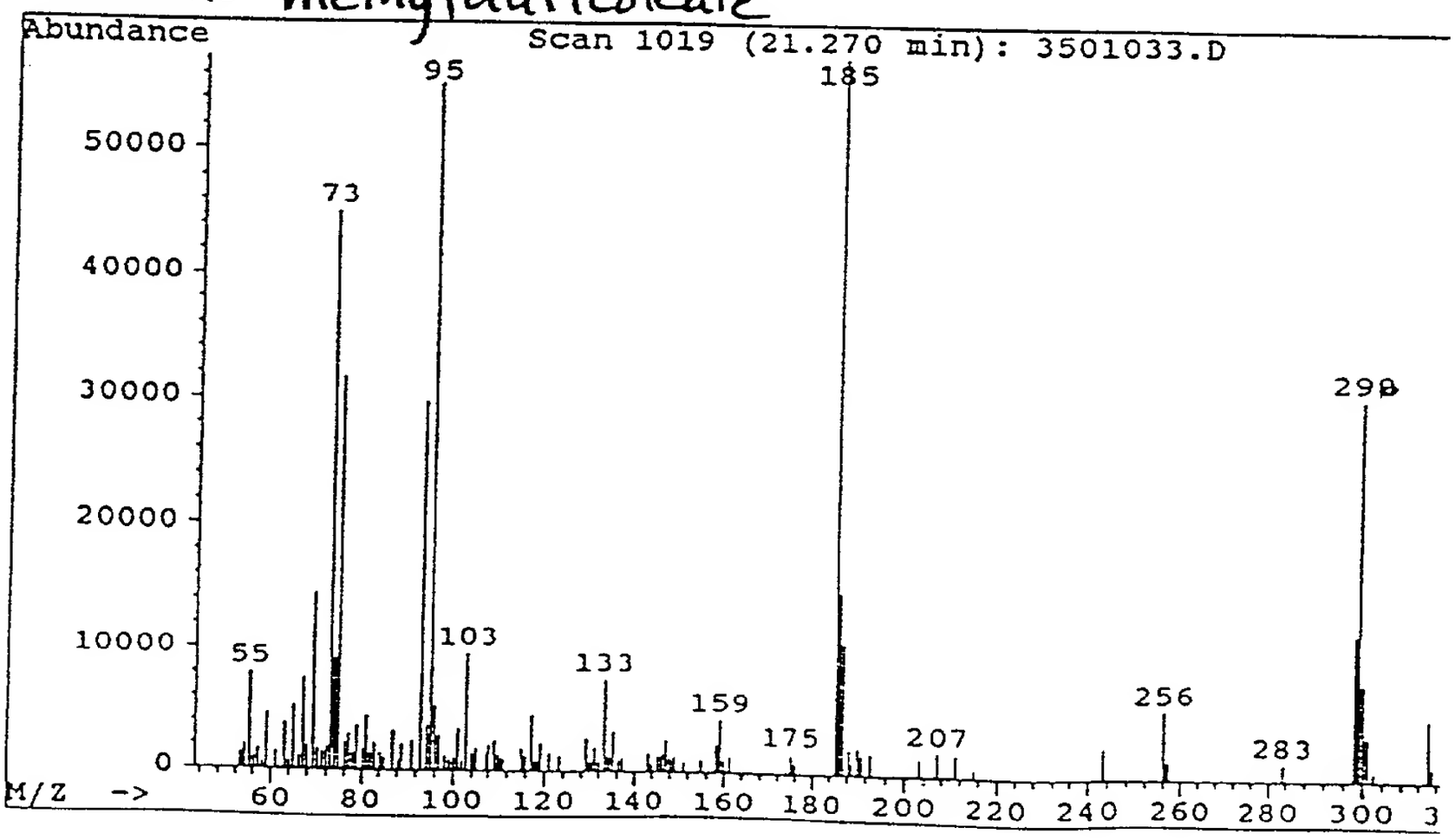
1C

O-TMS-methyl-lesqueroleate

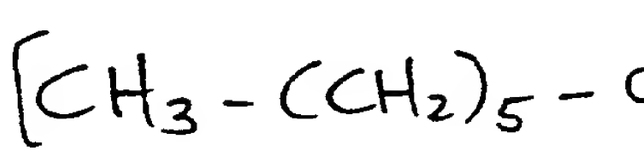



1D

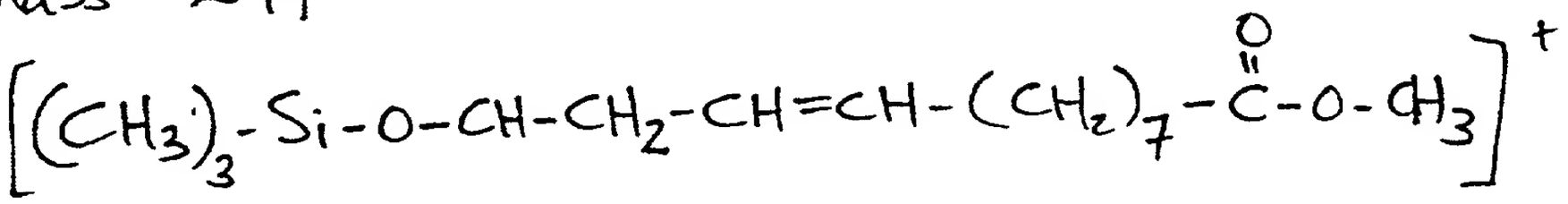
O-TMS-methyl auricoleate



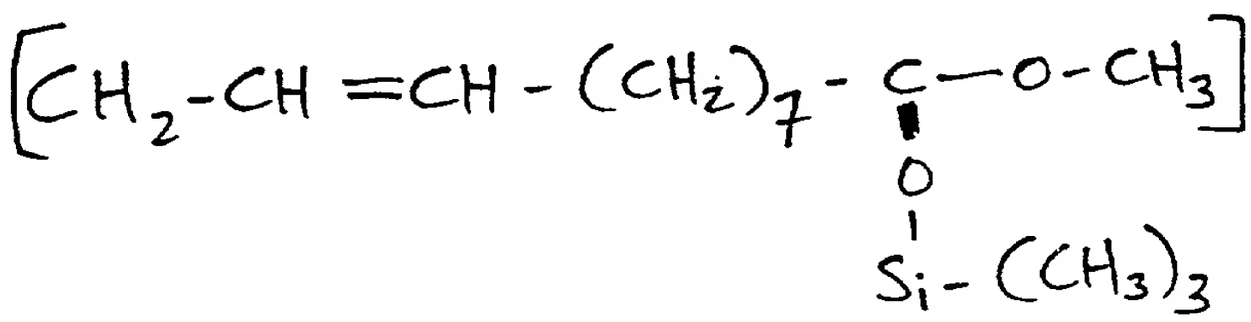
Ion#1: Mass 187



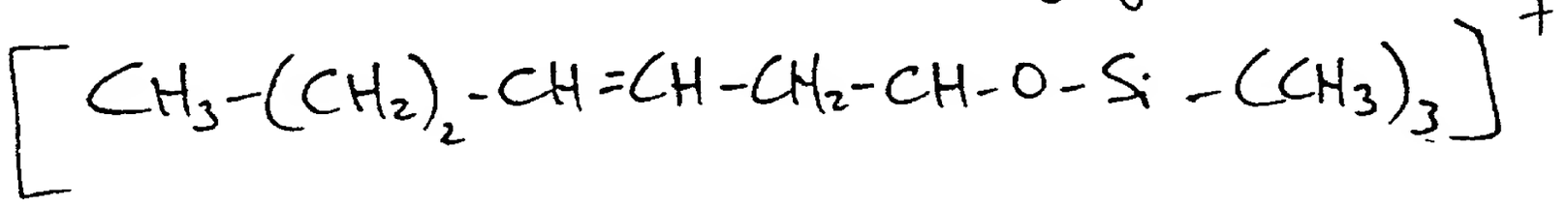
Ion#2: Mass 299



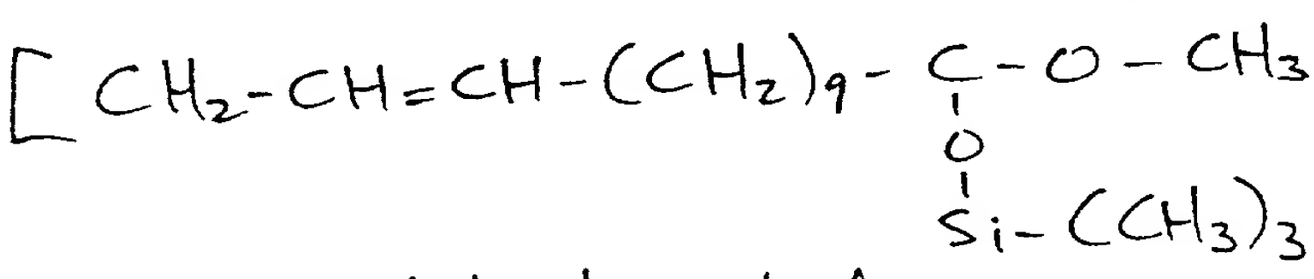
Ion#3: Mass 270 (characteristic rearrangement ion)



Ion#4: Mass 185 (desaturated analog of Ion #1)



Ion#5: Mass 298 (elongated analog of Ion#3)



Ion#6: Mass 327 (elongated analog of ion #2)

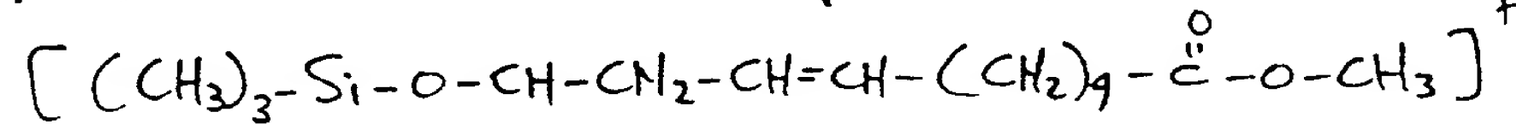


Figure 2.

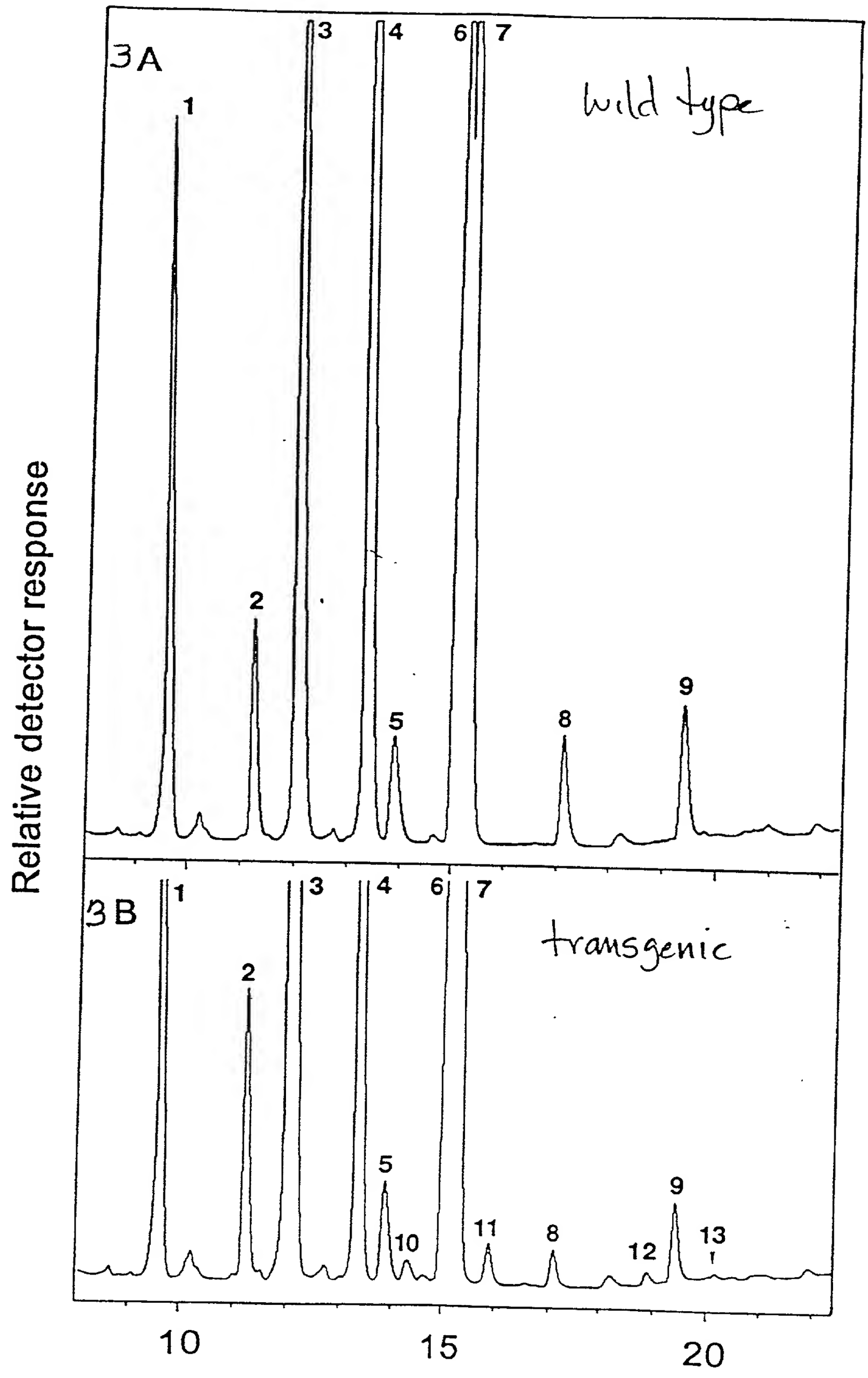
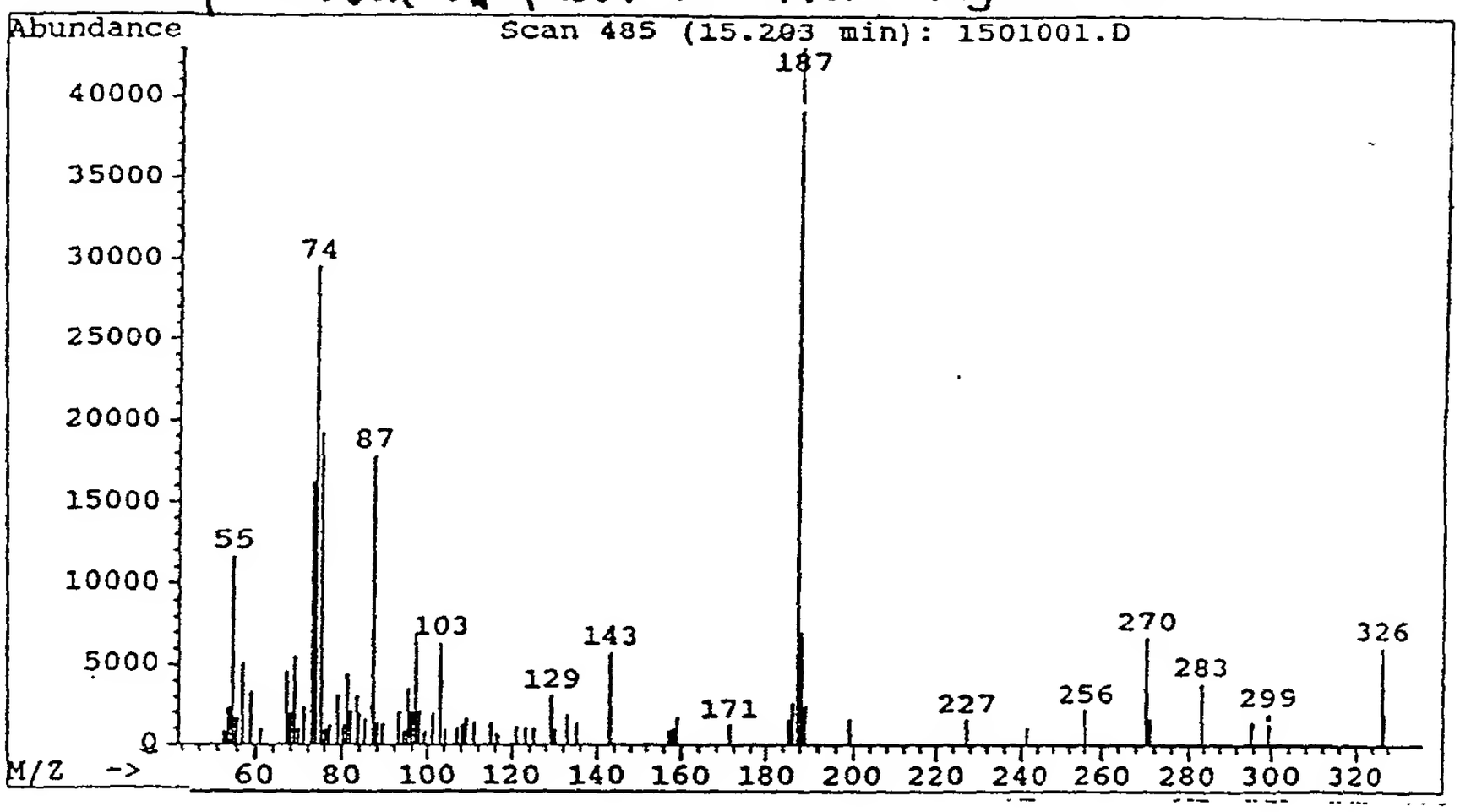

3A
1
2
3
4
5
6
7
8
9
wild type
Relative detector response
3B
1
2
3
4
5
6
7
8
9
10
11
12
13
transgenic
10
15
20
Elution time (min)

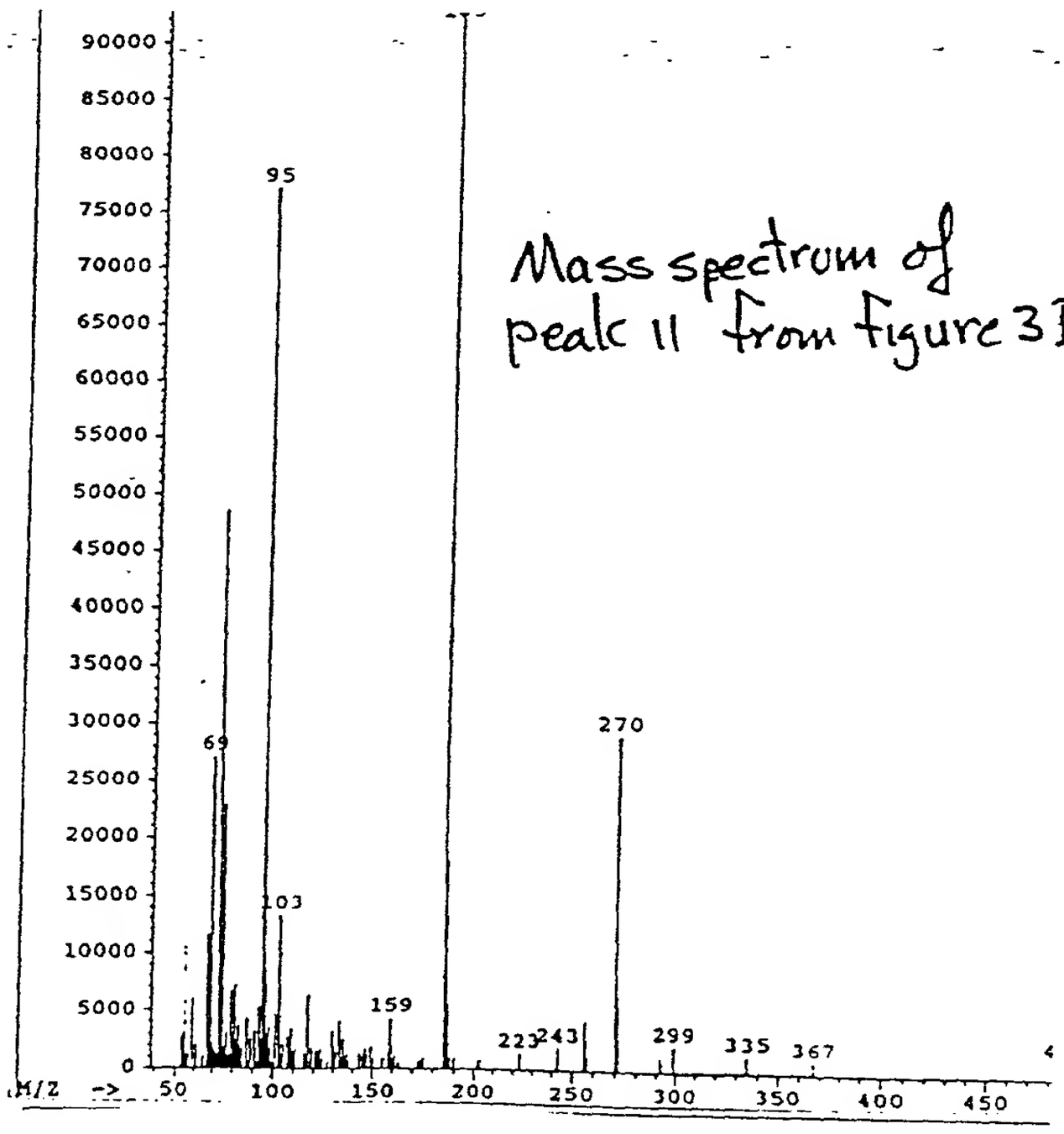
Figure 3

Figure 4A.

Mass Spectrum of peak 10 from figure 3B

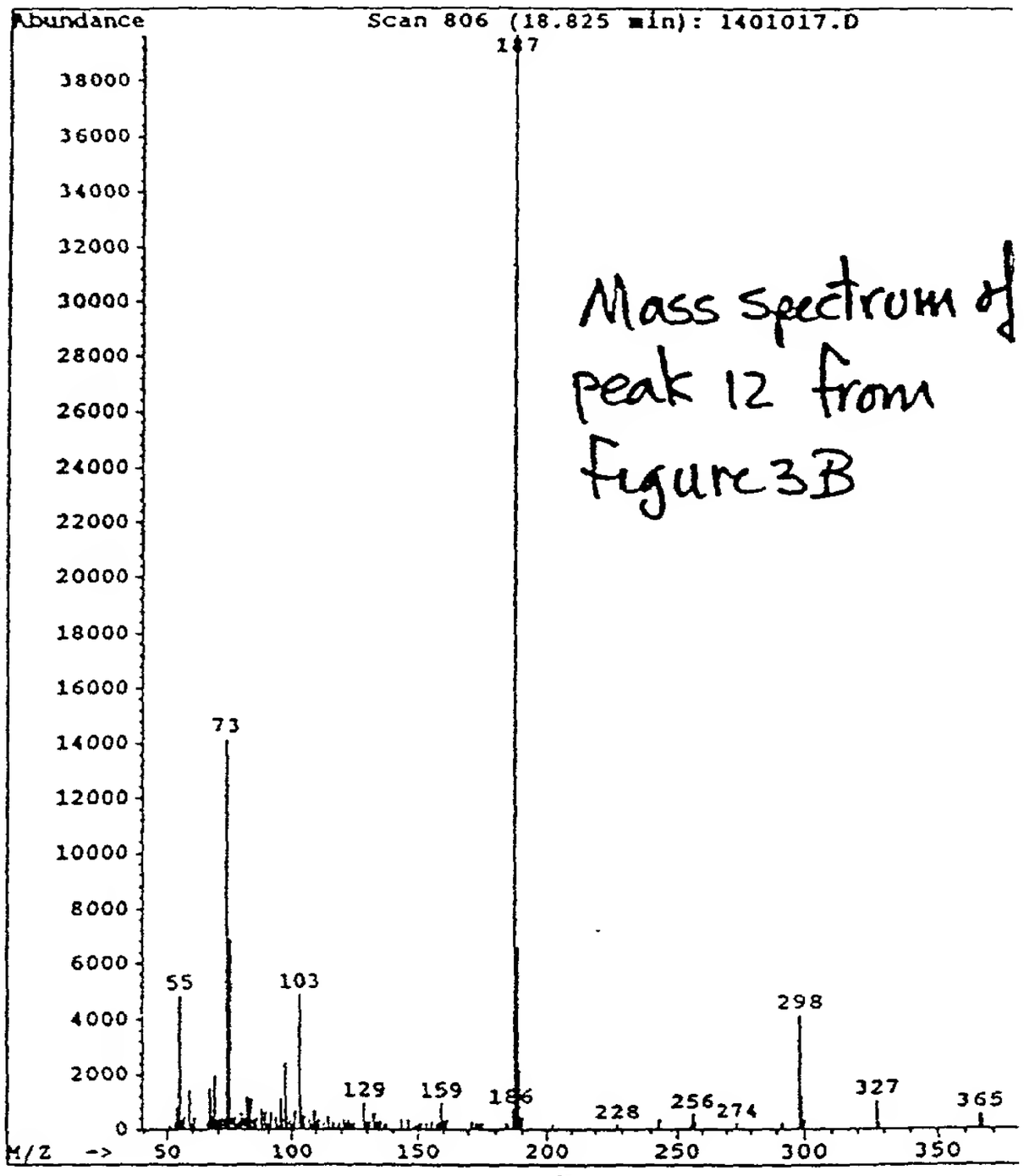



4B



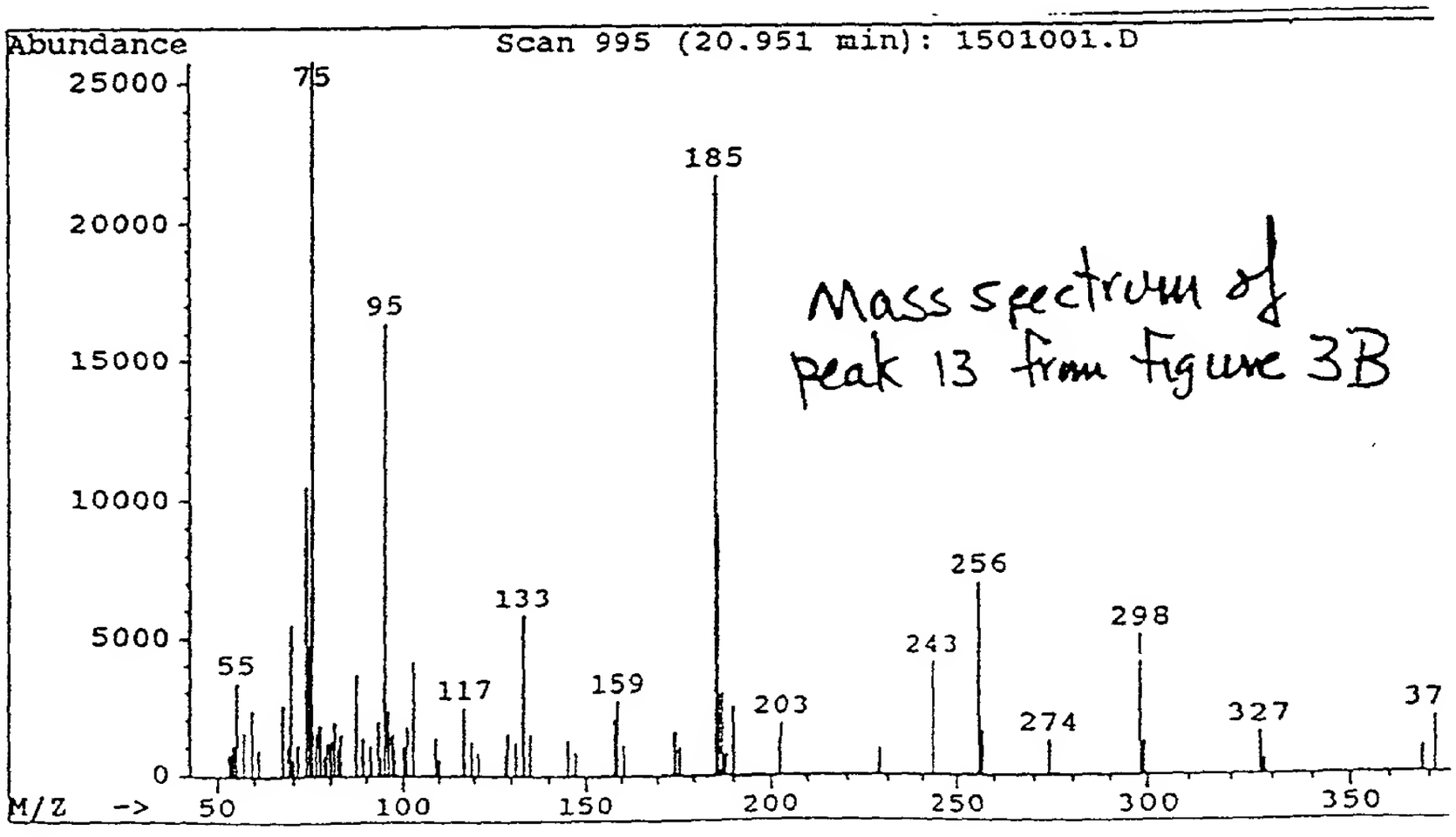

Mass spectrum of peak 11 from figure 3B

4C




Mass spectrum of peak 12 from Figure 3B

4D




Mass spectrum of peak 13 from Figure 3B

| 10 | 20 | 30 | 40 | 50 | 60 |
|---|---|---|---|---|---|
| TATTGGCACC | GGCGGCACCA | TTCCAACAAT | GGATCCCTAG | AAAAAGATGA | AGTCTTTGTC |
| 70 | 80 | 90 | 100 | 110 | 120 |
| CCACCTAAGA | AAGCTGCAGT | CANATGGTAT | GTCAAATACC | TCAACAACCC | TCTTGGACGC |
| 130 | 140 | 150 | 160 | 170 | 180 |
| ATTCTGGTGT | TAACAGTTCA | GTTTATCCTC | GGGTGGCCTT | TGTATCTAGC | CTTTAATGTA |
| 190 | 200 | 210 | 220 | 230 | 240 |
| TCAGGTAGAC | CTTATGATGG | TTTCGCTTCA | CATTTCTTCC | CTCATGCACC | TATCTTTAAG |
| 250 | 260 | 270 | 280 | 290 | 300 |
| GACCGTGAAC | GTCTCCAGAT | ATACATCTCA | GATGCTGGTA | TTCTAGCTGT | CTGTTATGGT |
| 310 | 320 | 330 | 340 | 350 | 360 |
| CTTTACCGTT | ACGCTGCTTC | ACAAGGATTG | ACTGCTATGA | TCTGCGTCTA | CGGAGTACCG |
| 370 | 380 | 390 | 400 | 410 | 420 |
| CTTTTGATAG | TGAACTTTTT | CCTTGTCTTG | GTCACTTTCT | TGCAGCACAC | TCATCCTTCA |
| 430 | 440 | 450 | 460 | 470 | 480 |
| TTACCTCACT | ATGATTCAAC | CGAGTGGGAA | TGGATTAGAG | GAGCTTTGGT | TACGGTAGAC |
| 490 | 500 | 510 | 520 | 530 | 540 |
| AGAGACTATG | GAATCTTGAA | CAAGGTGTTT | CACAACATAA | CAGACACCCA | CGTAGCACAC |
| 550 | | | | | |
| CAC | | | | | |

Figure 5 Nucleotide sequence of pLesq2

```
        10          20          30          40          50          60
TATAGGCACC  GGAGGCACCA  TTCCAACACA  GGATCCCTCG  AAAGAGATGA  AGTATTTGTC
        70          80          90         100         110         120
CCAAAGCAGA  AATCCGCAAT  CAAGTGGTAC  GGCGAATACC  TCAACAACCC  TCCTGGTCGC
       130         140         150         160         170         180
ATCATGATGT  TAACTGTCCA  GTTCGTCCTC  GGATGGCCCT  TGTACTTAGC  CTTCAACGTT
       190         200         210         220         230         240
TCTGGCAGAC  CCTACAATGG  TTTCGCTTCC  CATTTCTTCC  CCAATGCTCC  TATCTACAAC
       250         260         270         280         290         300
GACCGTGAAC  GCCTCCAGAT  TTACATCTCT  GATGCTGGTA  TTCTAGCCGT  CTGTTATGGT
       310         320         330         340         350         360
CTTTACCGTT  ACGCTGTTGC  ACAAGGACTA  GCCTCAATGA  TCTGTCTAAA  CGGAGTTCCG
       370         380         390         400         410         420
CTTCTGATAG  TTAACTTTTT  CCTCGTCTTG  ATCACTTACT  TACAACACAC  TCACCCTGCG
       430         440         450         460         470         480
TTGCCTCACT  ATGATTCATC  AGAGTGGGAT  TGGCTTAGAG  GAGCTTTAGC  TACTGTAGAC
       490         500         510         520         530         540
AGAGACTATG  GAATCTTGAA  CAAGGTGTTC  CATAACATCA  CAGACACCCA  CGTCGCACAC
       550
CACT
```

Figure 6 Nucleotide sequence of pLesq3

Probe pLesq3

Probe pLesq2

S L S L

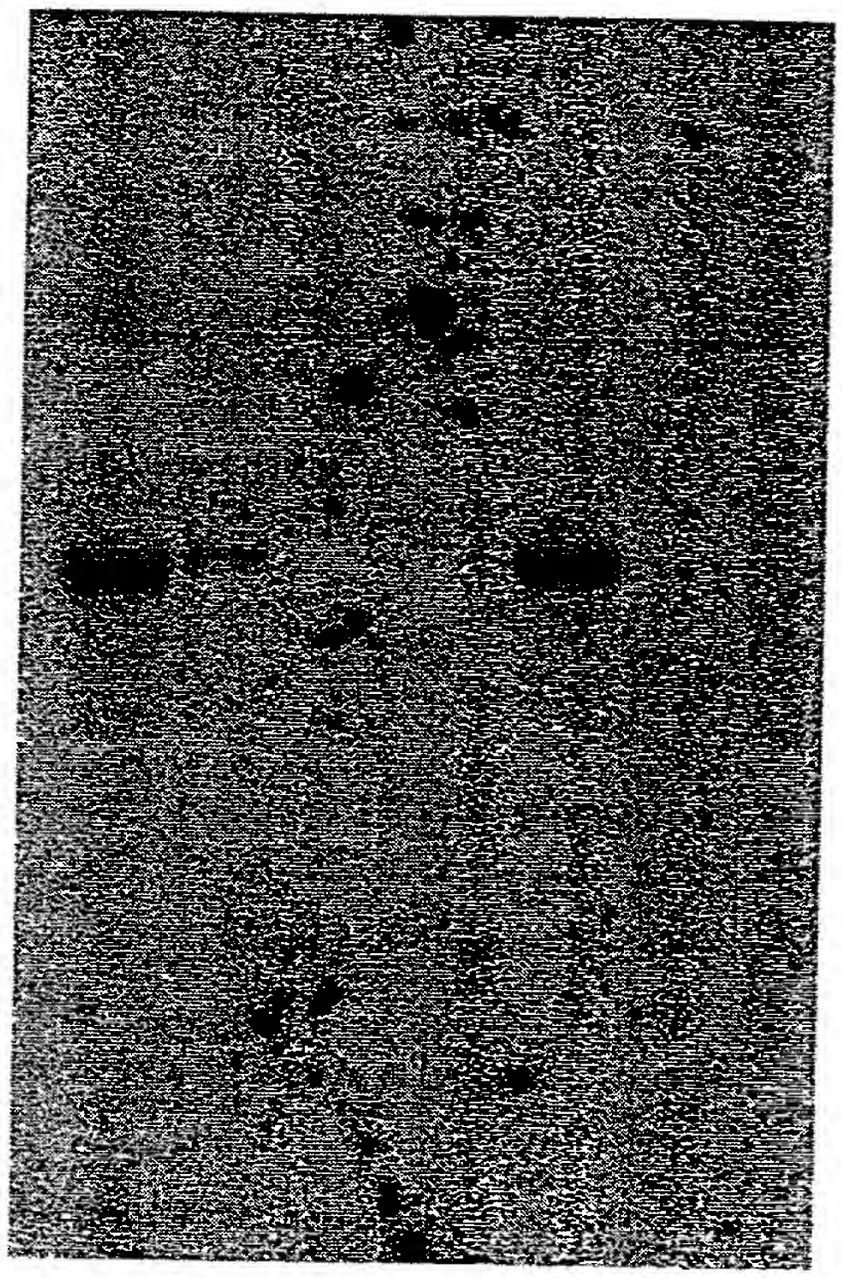


Figure 7

```
                                                                        AT GAA GCT TTA TAA GAA GTT AGT TTT CTC TGG TGA CAG AGA AAT TNT      47

GTC AAT TGG TAG TGA CAG TTG AAG CAA CAG GAA CAA CAA GGA TGG TTG      95

GTG NTG ATG CTG ATG TGG TGA TGT GTT ATT CAT CAA ATA CTA AAT ACT     143

ACA TTA CTT GTT GCT GCC TAC TTC TCC TAT TTC CTC CGC CAC CCA TTT     191

TGG ACC CAC GAN CCT TCC ATT TAA ACC CTC TCT CGT GCT ATT CAC CAG     239

AAG AGA AGC CAA GAG AGA GAG AGA GAG AAT GTT CTG AGG ATC ATT GTC     287

TTC TTC ATC GTT ATT AAC GTA AGT TTT TTT TGA CCA CTC ATA TCT AAA     335

ATC TAG TAC ATG CAA TAG ATT AAT GAC TGT TCC TTC TTT TGA TAT TTT     383

                                  Met Gly Ala Gly Gly Arg Ile Met Val Thr      10
CAG CTT CTT GAA TTC AAG ATG GGT GCT GGT GGA AGA ATA ATG GTT ACC     431

Pro Ser Ser Lys Lys Ser Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys      26
CCC TCT TCC AAG AAA TCA GAA ACT GAA GCC CTA AAA CGT GGA CCA TGT     479

Glu Lys Pro Pro Phe Thr Val Lys Asp Leu Lys Lys Ala Ile Pro Gln      42
GAG AAA CCA CCA TTC ACT GTT AAA GAT CTG AAG AAA GCA ATC CCA CAG     527

His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr      58
CAT TGT TTC AAG CGC TCT ATC CCT CGT TCT TTC TCC TAC CTT CTC ACA     575

Asp Ile Thr Leu Val Ser Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe      74
GAT ATC ACT TTA GTT TCT TGC TTC TAC TAC GTT GCC ACA AAT TAC TTC     623

Ser Leu Leu Pro Gln Pro Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr      90
TCT CTT CTT CCT CAG CCT CTC TCT ACT TAC CTA GCT TGG CCT CTC TAT     671

Trp Val Cys Gln Gly Cys Val Leu Thr Gly Ile Trp Val Ile Gly His     106
TGG GTA TGT CAA GGC TGT GTC TTA ACC GGT ATC TGG GTC ATT GGC CAT     719

Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr     122
GAA TGT GGT CAC CAT GCA TTC AGT GAC TAT CAA TGG GTA GAT GAC ACT     767

Val Gly Phe Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp     138
GTT GGT TTT ATC TTC CAT TCC TTC CTT CTC GTC CCT TAC TTC TCC TGG     815

Lys Tyr Ser His Arg Arg His His Ser Asn Asn Gly Ser Leu Glu Lys     154
AAA TAC AGT CAT CGT CGT CAC CAT TCC AAC AAT GGA TCT CTC GAG AAA     863

Asp Glu Val Phe Val Pro Pro Lys Lys Ala Ala Val Lys Trp Tyr Val     170
GAT GAA GTC TTT GTC CCA CCG AAG AAA GCT GCA GTC AAA TGG TAT GTT     911

Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Leu Val Leu Thr Val Gln     186
AAA TAC CTC AAC AAC CCT CTT GGA CGC ATT CTG GTG TTA ACA GTT CAG     959
```

Figure 8A

```
Phe Ile Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg     202
TTT ATC CTC GGG TGG CCT TTG TAT CTA GCC TTT AAT GTA TCA GGT AGA    1007

Pro Tyr Asp Gly Phe Ala Ser His Phe Phe Pro His Ala Pro Ile Phe     218
CCT TAT GAT GGT TTC GCT TCA CAT TTC TTC CCT CAT GCA CCT ATC TTT    1055

Lys Asp Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu     234
AAA GAC CGA GAA CGC CTC CAG ATA TAC ATC TCA GAT GCT GGT ATT CTA    1103

Ala Val Cys Tyr Gly Leu Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr     250
GCT GTC TGT TAT GGT CTT TAC CGT TAC GCT GCT TCA CAA GGA TTG ACT    1151

Ala Met Ile Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Phe Phe     266
GCT ATG ATC TGC GTC TAT GGA GTA CCG CTT TTG ATA GTG AAC TTT TTC    1199

Leu Val Leu Val Thr Phe Leu Gln His Thr His Pro Ser Leu Pro His     282
CTT GTC TTG GTA ACT TTC TTG CAG CAC ACT CAT CCT TCG TTA CCT CAT    1247

Tyr Asp Ser Thr Glu Trp Glu Trp Ile Arg Gly Ala Leu Val Thr Val     298
TAT GAT TCA ACC GAG TGG GAA TGG ATT AGA GGA GCT TTG GTT ACG GTA    1295

Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp     314
GAC AGA GAC TAT GGA ATA TTG AAC AAG GTG TTC CAT AAC ATA ACA GAC    1343

Thr His Val Ala His His Leu Phe Ala Thr Ile Pro His Tyr Asn Ala     330
ACA CAT GTG GCT CAT CAT CTC TTT GCA ACT ATA CCG CAT TAT AAC GCA    1391

Met Glu Ala Thr Glu Ala Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His     346
ATG GAA GCT ACA GAG GCG ATA AAG CCA ATA CTT GGT GAT TAC TAC CAC    1439

Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu     362
TTC GAT GGA ACA CCG TGG TAT GTG GCC ATG TAT AGG GAA GCA AAG GAG    1487

Cys Leu Tyr Val Glu Pro Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr     378
TGT CTC TAT GTA GAA CCG GAT ACG GAA CGT GGG AAG AAA GGT GTC TAC    1535

Tyr Tyr Asn Asn Lys Leu                                            384
TAT TAC AAC AAT AAG TTA TGA GGC TGA TAG GGC GAG AGA AGT GCA ATT    1583

ATC AAT CTT CAT TTC CAT GTT TTA GGT GTC TTG TTT AAG AAG CTA TGC    1631

TTT GTT TCA ATA ATC TCA GAG TCC ATN TAG TTG TGT TCT GGT GCA TTT    1679

TGC CTA GTT ATG TGG TGT CGG AAG TTA GTG TTC AAA CTG CTT CCT GCT    1727

GTG CTG CCC AGT GAA GAA CAA GTT TAC GTG TTT AAA ATA CTC GGA ACG    1775

AAT TGA CCA CAA NAT ATC CAA AAC CGG CTA TCC GAA TTC CAT ATC CGA    1823

AAA CCG GAT ATC CAA ATT TCC AGA GTA CTT AG                        1855
```

Figure 8B

```
                                10        20        30        40        50
LFFAH12.AMI           1 MGAGGRIM-- --VTPSSKKS --ETEALKRG PCEKPPFTVK DLKKAIPQHC          50
FAH12.AMI             1 MGGGGRMSTV ITSNNSEKKG --GSSHLKRA PHTKPPFTLG DLKRAIPPHC          50
ATFAD2.AMI            1 MGAGGRMP-- --VPTSSKKS --ETDTTKRV PCEKPPFSVG DLKKAIPPHC          50
BNFAD2.AMI            1 MGAGGRMQ-- --VSPPSKKS --ETDNIKRV PCETPPFTVG ELKKAIPPHC          50
    D2-1.AMI          1 MGLA-KETTM GGRGRVAKVE VQGKKPLSRV PNTKPPFTVG QLKKAIPPHC          50
GMFAD2-2.AMI          1 MGAGGR---- TDVPPANRKS --EVDPLKRV PFEKPQFSLS QIKKAIPPHC          50
ZMFAD2.AMI            1 MGAGGRMTEK EREKQEQLAR ATGGAAMQRS PVEKPPFTLG QIKKAIPPHC          50
RCFAD2.AMI            1 ---------- ---------- ---------- ---------- ----------          50
                                60        70        80        90       100
LFFAH12.AMI          51 FKRSIPRSFS YLLTDITLVS CFYYVATNYF SLLPQPLSTY LAWPLYWVCQ         100
FAH12.AMI            51 FERSFVRSFS YVAYDVCLSF LFYSIATNFF PYISSPLS-Y VAWLVYWLFQ         100
ATFAD2.AMI           51 FKRSIPRSFS YLISDIIIAS CFYYVATNYF SLLPQPLS-Y LAWPLYWACQ         100
BNFAD2.AMI           51 FKRSIPRSFS HLIWDIIIAS CFYYVATTYF PLLPNPLS-Y FAWPLYWACQ         100
GMFAD2-1.AMI         51 FQRSLLTSFS YVVYDLSRAF IFY-IATTYF HLLPQPFS-L IAWPIYWVLQ         100
GMFAD2-2.AMI         51 FQRSVLRSFS YVVYDLTIAF CLYYVATHYF HLLPGPLS-F RGMAIYWAVQ         100
ZMFAD2.AMI           51 FERSVLKSFS YVVHDLVIAA ALLYFALAII PALPSPLR-Y AAWPLYWIAQ         100
RCFAD2.AMI           51 ---------- ---------- ---------- ---------- ----------         100
                               110       120       130       140       150
LFFAH12.AMI         101 GCVLTGIWVI GHECGHHAFS DYQWVDDTVG FIFHSFLLVP YFSWKYSHRR         150
FAH12.AMI           101 GCILTGLWVI GHECGHHAFS EYQLADDIVG LIVHSALLVP YFSWKYSHRR         150
ATFAD2.AMI          101 GCVLTGIWVI AHECGHHAFS DYQWLDDTVG LIFHSFLLVP YFSWKYSHRR         150
BNFAD2.AMI          101 GCVLTGVWVI AHECGHAAFS DYQWLDDTVG LIFHSFLLVP YFSWKYSHRR         150
GMFAD2-1.AMI        101 GCLLTGVWVI AHECGHHAFS KYQWVDDVVG LTLHSTLLVP YFSWKISHRR         150
GMFAD2-2.AMI        101 GCILTGVWVI AHECGHHAFS DYQLLDDIVG LILHSALLVP YFSWKYSHRR         150
ZMFAD2.AMI          101 G---------  -------AFS DYSLLDDVVG LVLHSSLMVP YFSWKYSHRR         150
RCFAD2.AMI          101 -------WVM AHDCGHHAFS DYQLLDDVVG LILHSCLLVP YFSWKHSHRR         150
                               160       170       180       190       200
LFFAH12.AMI         151 HHSNTGSLEK DEVFVPPKKA AVKWYVKYL- NNPLGRILVL TVQFILGWPL         200
FAH12.AMI           151 HHSNIGSLER DEVFVPKSKS KISWYSKYS- NNPPGRVLTL AATLLLGWPL         200
ATFAD2.AMI          151 HHSNIGSLER DEVFVPKQKS AIKWYGKYL- NNPLGRIMML TVQFVLGWPL         200
BNFAD2.AMI          151 HHSNIGSLER DEVFVPR-RS QTSSGTAST- STTFGRTVML TVQFTLGWPL         200
GMFAD2-1.AMI        151 HHSNIGSLDR DEVFVPKPKS KVAWFSKYL- NNPLGRAVSL LVTLTIGWPM         200
GMFAD2-2.AMI        151 HHSNIGSLER DEVFVPKQKS CIKWYSKYL- NNPPGRVLTL AVTLTLGWPL         200
ZMFAD2.AMI          151 HHSNIGSLER DEVFVPKKKE ALPWYTPYVY NNPVGRVVHI VVQLTLGWPL         200
RCFAD2.AMI          151 HHSNIGSLER DEVFVPKKKS SIRWYSKYL- NNPPGRIMTI AVTLSLGWPL         200
                               210       220       230       240       250
LFFAH12.AMI         201 YLAFNVSGRP YDG-FASHFF PHAPIFKDRE RLQIYISDAG ILAVCYGLYR         250
FAH12.AMI           201 YLAFNVSGRP YDR-FACHYD PYGPIFSERE RLQIYIADLG IFATTFVLYQ         250
ATFAD2.AMI          201 YLAFNVSGRP YDG-FACHFF PNAPIYNDRE RLQIYLSDAG ILAVCFGLYR         250
BNFAD2.AMI          201 YLAFNVSGRP YDGGFACHFH PNAPIYNDRE RLQIYISDAG ILAVCYGLLP         250
GMFAD2-1.AMI        201 YLAFNVSGRP YDS-FASHYH PYAPIYSNRE RLLIYVSDVA LFSVTYSLYR         250
GMFAD2-2.AMI        201 YLALNVSGRP YDR-FACHYD PYGPIYSDRE RLQIYISDAG VLAVVYGLFR         250
ZMFAD2.AMI          201 YLATNASGRP YPR-FACHFD PYGPIYNDRE RAQIFVSDAG VVAVAFGLYK         250
RCFAD2.AMI          201 YLAFNVSGRP YDR-FACHYD PYGPIYNDRE RIEIFISDAG VLAVTFGLYQ         250
                               260       270       280       290       300
LFFAH12.AMI         251 YAASQGLTAM ICVYGVPLLI VNFFLVLVTF LQHTHPSLPH YDSTEWEWIR         300
FAH12.AMI           251 ATMAKGLAWV MRIYGVPLLI VNCFLVMITY LQHTHPAIPR YGSSEWDWLR         300
ATFAD2.AMI          251 YAAAQGMASM ICLYGVPLLI VNAFLVLITY LQHTHPSLPH YDSSEWDWLR         300
BNFAD2.AMI          251 YAAVQGVASM VCFLRVPLLI VNGFLVLITY LQHTHPSLPH YDSSEWDWLR         300
GMFAD2-1.AMI        251 VATLKGLVWL LCVYGVPLLI VNGFLVTITY LQHTHFALPH YDSSEWDWLK         300
    AD2-2.AMI       251 LAMAKGLAWV VCVYGVPLLV VNGFLVLITF LQHTHPALPH YTSSEWDWLR         300
ZMFAD2.AMI          251 LAAAFGVWWV VRVYAVPLLI VNAWLVLITY LQHTHPSLPH YDSSEWDWLR         300
```

Figure 9A

```
RCFAD2.AMI      251 LAIAKGLAWV VCVYGVPLLV VNSFLVLITF LQHTHPALPH YDSSEWDWLR      300
                          310        320        330        340        350
LFFAH12.AMI     301 GALVITVDRDY GILNKVFHNI TDTHVAHHLF ATIPHYNAME ATEAIKPILG      350
FAH12.AMI       301 GAMVITVDRDY GVLNKVFHNI ADTHVAHHLF AIVPHYHAME ATKAIKPIMG      350
   .D2.AMI      301 GALATVDRDY GILNKVFHNI TDTHVAHHLF SIMPHYNAME ATKAIKPILG      350
BNFAD2.AMI      301 GALATVDRDY GILNQGFHNI TDTHEAHHLF SIMPHYHAME ATKAIKPILG      350
GMFAD2-1.AMI    301 GALATMDRDY GILNKVFHHI TDTHVAHHLF SIMPHYHAME ATNAIKPILG      350
GMFAD2-2.AMI    301 GALATVDRDY GILNKVFHNI TDTHVAHHLF SIMPHYHAME ATKAIKPILG      350
ZMFAD2.AMI      301 GALATMDRDY GILNRVFHNI TDTHVAHHLF SIMPHYHAME ATKAIRPILG      350
RCFAD2.AMI      301 GALATVDRDY GILNKVFHNI TDTQVAHHLF -TMP------ ----------      350
                          360        370        380        390        400
LFFAH12.AMI     351 DYYHFDGTPW YVAMYREAKE CLYVEPDTER GKKGVYYYNN K-L.......      400
FAH12.AMI       351 EYYRYDGTPF YKALWREAKE CLFVEPDEGA PTQGVFWYRN KY-.......      400
ATFAD2.AMI      351 DYYQFDGTPW YVAMYREAKE CIYVEPDREG DKKGVYWYNN K-L.......      400
BNFAD2.AMI      351 EYYQFDGTPV VKAMWREAKE CIYVEPDRQG EKKGVFWYNN KL*.......      400
GMFAD2-1.AMI    351 EYYQFDDTPF YKALWREARE CLYVEPDEGT SEKGVYWYRN KY-.......      400
GMFAD2-2.AMI    351 EYYRFDETPF VKAMWREARE CIYVEPDQST ESKGVFWYNN KL-.......      400
ZMFAD2.AMI      351 DYYHFDPTPV AKATWREAGE CIYVEPE--- DRKGVFWYNK KF*.......      400
RCFAD2.AMI      351 ---------- ---------- ---------- ---------- ---.......      400
                          410        420        430        440        450
LFFAH12.AMI     401 .......... .......... .......... .......... ..........      450
FAH12.AMI       401 .......... .......... .......... .......... ..........      450
ATFAD2.AMI      401 .......... .......... .......... .......... ..........      450
BNFAD2.AMI      401 .......... .......... .......... .......... ..........      450
GMFAD2-1.AMI    401 .......... .......... .......... .......... ..........      450
GMFAD2-2.AMI    401 .......... .......... .......... .......... ..........      450
ZMFAD2.AMI      401 .......... .......... .......... .......... ..........      450
```

Figure 9B

Molecular weight markers

E H X

3.6 –

1.8 –

1.5 –

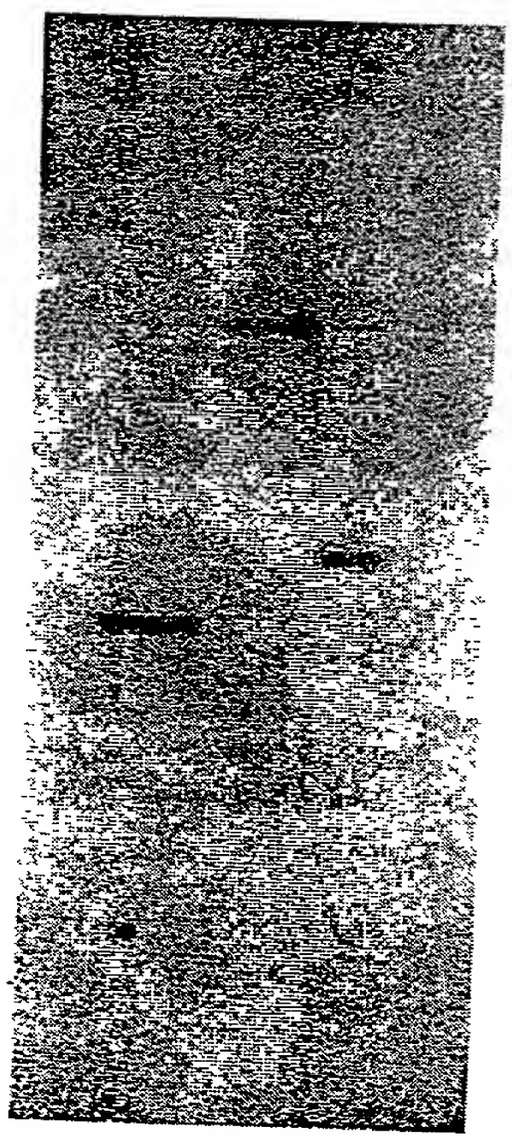


Figure 10

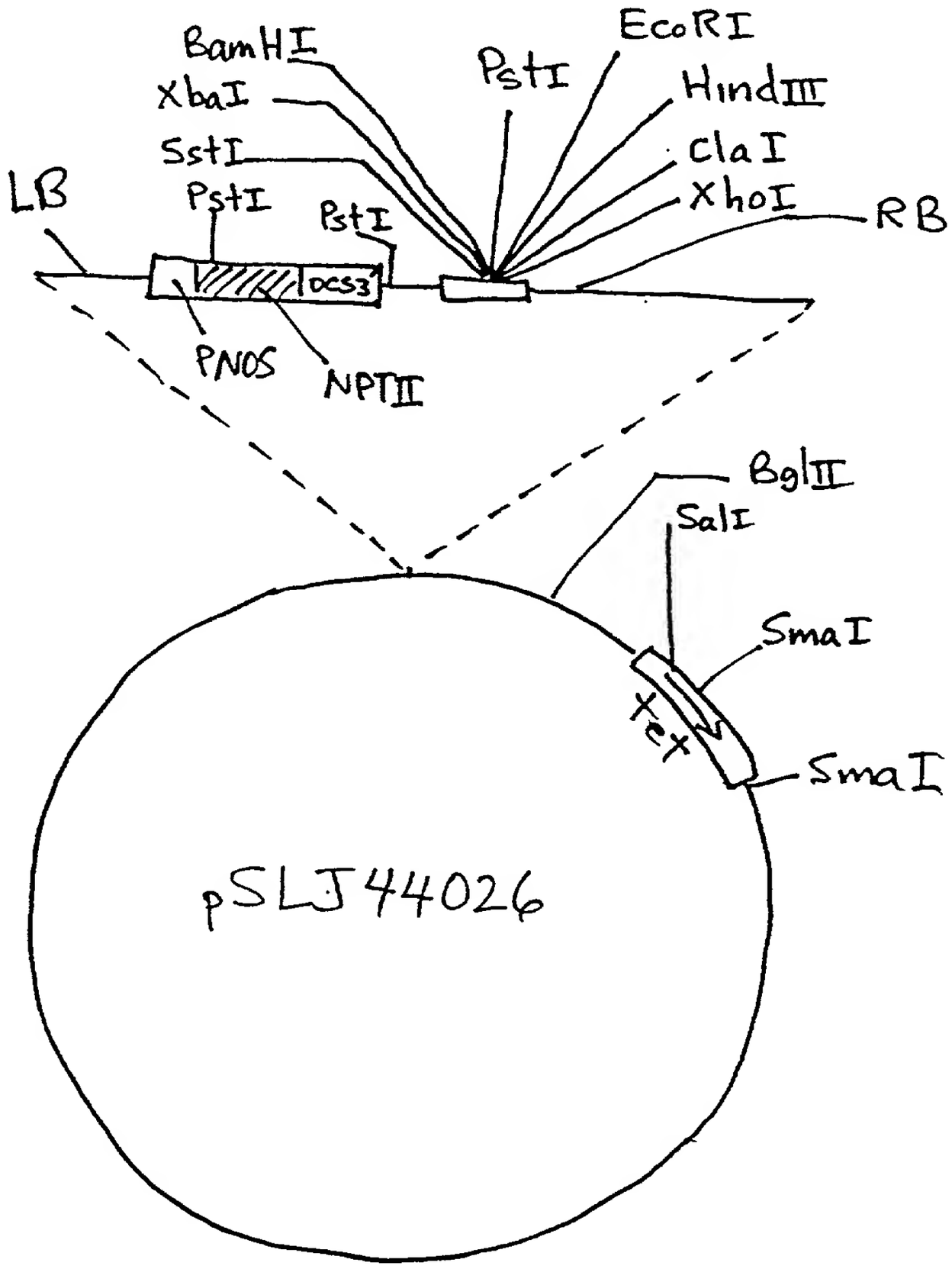

BamHI
XbaI
SstI
PstI
PstI
LB
OCS3
PNOS
NPTII
PstI
EcoRI
HindIII
ClaI
XhoI
RB
BglII
SalI
SmaI
tet
SmaI
pSLJ44026

Figure 11